GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2004, 10:41:53 ; Search time 54 Seconds
(without alignments)
423.821 Million cell updates/sec

Title: US-09-856-840C-2
Perfect score: 473
Sequence: 1 MFLLVFLCCLHLVISSHTPD.........VEWVPYSTGQCRTTCIPTVG 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 453 | 95.8 | 81 | 3 | AAY92938 | Aay92938 Hirudo me |
| 2 | 79 | 16.7 | 145 | 4 | AAM87949 | Aam87949 Human imm |
| 3 | 76 | 16.1 | 19938 | 6 | ABP76678 | Abp76678 Streptomy |
| 4 | 75.5 | 16.0 | 355 | 5 | ABP69588 | Abp69588 Human pol |
| 5 | 75.5 | 16.0 | 355 | 5 | AAU97101 | Aau97101 Human MK6 |
| 6 | 75.5 | 16.0 | 355 | 7 | ADC37275 | Adc37275 Nuclear f |
| 7 | 75.5 | 16.0 | 380 | 5 | AAU97114 | Aau97114 Human MK6 |
| 8 | 75 | 15.9 | 294 | 5 | ABP95622 | Abp95622 Human GPC |
| 9 | 74.5 | 15.8 | 136 | 5 | AAU97103 | Aau97103 Human MK6 |
| 10 | 73.5 | 15.5 | 105 | 7 | ADC31222 | Adc31222 Human nov |
| 11 | 73 | 15.4 | 515 | 2 | AAR48670 | Aar48670 Chitinase |
| 12 | 72 | 15.2 | 1083 | 4 | ABB60057 | Abb60057 Drosophil |
| 13 | 71.5 | 15.1 | 56 | 4 | AAM37769 | Aam37769 Drosophil |
| 14 | 71.5 | 15.1 | 56 | 4 | AAM77584 | Aam77584 Peptide # |
| 15 | 71.5 | 15.1 | 56 | 4 | AAM64835 | Aam64835 Human bra |
| 16 | 71.5 | 15.1 | 56 | 4 | ABG59231 | Abg59231 Human bon |
| 17 | 71.5 | 15.1 | 85 | 5 | AAU97102 | Aau97102 Human liv |
| 18 | 71.5 | 15.1 | 113 | 4 | ABG30035 | Abg30035 Human MK6 |
| 19 | 71 | 15.0 | 761 | 4 | ABB60973 | Abb60973 Novel hum |
| 20 | 68.5 | 14.5 | 82 | 4 | AAU57028 | Aau57028 Drosophil |
| 21 | 68.5 | 14.5 | 82 | 6 | ABM53547 | Abm53547 Propionib |
| 22 | 68.5 | 14.5 | 727 | 2 | AAR05533 | Aar05533 Propionib |
| 23 | 68.5 | 14.5 | 1214 | 3 | AAY79152 | Aay79152 Fragment |
| 24 | 68.5 | 14.5 | 19938 | 6 | ABB98398 | Abb98398 Mouse pro |
| 25 | 68 | 14.4 | 100 | 4 | AAW48795 | Aaw48795 Streptomy |
| 26 | 68 | 14.4 | 197 | 4 | ABB12460 | Abb12460 Homo sapi |
| 27 | 68 | 14.4 | 288 | 4 | ABB12377 | Abb12377 Human bon |
| 28 | 68 | 14.4 | 288 | 4 | ABO07186 | Abo07186 Human bon |
| 29 | 68 | 14.4 | 934 | 5 | AAU72893 | Aau72893 Human p53 |
| 30 | 68 | 14.4 | 1964 | 4 | AAW95557 | Aaw95557 Human met |
| 31 | 67.5 | 14.3 | 74 | 4 | AAO10231 | Aao10231 Mus muscu |
| 32 | 67.5 | 14.3 | 325 | 3 | AAG60058 | Aag60058 Human pol |
| 33 | 67.5 | 14.3 | 548 | 7 | ADC87345 | Adc87345 Arabidops |
| 34 | 67.5 | 14.3 | 1872 | 2 | AAW68510 | Aaw68510 Human GPC |
| 35 | 67.5 | 14.3 | 2321 | 2 | AAW49698 | Aaw49698 Partial h |
| 36 | 67.5 | 14.2 | 227 | 2 | AAY17648 | Aay17648 Human Not |
| 37 | 67 | 14.2 | 227 | 2 | ADB17578 | Adb17578 Human put |
| 38 | 67 | 14.2 | 228 | 2 | AAY17679 | Aay17679 Amino aci |
| 39 | 67 | 14.2 | 228 | 2 | ADB17636 | Adb17636 Human WIS |
| 40 | 67 | 14.2 | 229 | 2 | AAY17678 | Aay17678 Human WIS |
| 41 | 67 | 14.2 | 229 | 6 | ADB17635 | Adb17635 Human WIS |
| 42 | 67 | 14.2 | 230 | 2 | AAY17677 | Aay17677 Human WIS |
| 43 | 67 | 14.2 | 230 | 6 | ADB17634 | Adb17634 Human WIS |
| 44 | 67 | 14.2 | 231 | 2 | AAY17676 | Aay17676 Human WIS |
| 45 | 67 | 14.2 | 231 | 6 | ADB17633 | Adb17633 Human WIS |

ALIGNMENTS

RESULT 1
AAY92938

ID    AAY92938 standard; protein; 81 AA.
XX
AC    AAY92938;
XX
DT    08-NOV-2000  (first entry)
XX
DE    Hirudo medicinalis metallocarboxypeptidase inhibitor protein.
XX
KW    Recombinant; leech; metallocarboxypeptidase inhibitor; fibrin;
KW    plasma carboxypeptidase B; fibrinolysis inhibitor; plasminogen;
KW    blood clot.
XX
OS    Hirudo medicinalis.
XX

```
FH      Key                 Location/Qualifiers
FT      Peptide             1..15
FT                          /note= "signal peptide"
FT      Protein             16..81
FT                          /note= "mature metallocarboxypeptidase inhibitor"
FT
XX
PN      WO200031140-A1.
XX
PD      02-JUN-2000.
XX
PF      24-NOV-1999;    99WO-ES000378.
XX
PR      25-NOV-1998;    98ES-00002524.
XX
PA      (UYBA-) UNIV AUTONOMA BARCELONA.
PA      (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
XX
PI      Reverter D, Vendrell J, Canals F, Horstmann J, Querol E, Fritz H;
PI      Sommerhoff CP, Aviles FX;
XX
DR      WPI; 2000-400047/34.
DR      N-PSDB; AAA11268.
XX
PT      New recombinant nucleic acid encoding metallocarboxypeptidase inhibitor,
PT      useful as fibrinolytic agent, is derived from the leech Hirudo
PT      medicinalis.
XX
PS      Claim 3; Page 17; 23pp; Spanish.
XX
CC      This sequence represents a protein derived from Hirudo medicinalis
CC      (leeches) that inhibits metallocarboxypeptidases, particularly of plasma
CC      carboxypeptidase B which inhibits fibrinolysis by destroying the binding
CC      site, in plasminogen, for fibrin. The inhibitor is useful as a
CC      fibrinolytic agent, thus promotes activity of plasminogen and speeds up
CC      lysis of blood clots
XX
SQ      Sequence 81 AA;

Query Match             95.8%;  Score 453;  DB 3;  Length 81;
Best Local Similarity   97.5%;  Pred. No. 2.1e-39;
Matches   78;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy          1 MFLLVFLCCLHLVISSHTPDESFLCTCQPDQVCCPICRGAAPLPSEGECNPHPTAPWCREG 60
              |||||||||||||||||||| ||||| |||||||||||||||||||||||||||||||||||
Db          1 MFLLVFLCCLHLVISSHTPDESFLCYCQPDQVCCPICRGAAPLPSEGECNPHPTAPWCREG 60

Qy         61 AVEWVPYSTGQCRTTCIPTV 80
              ||||||||||||||||||||
Db         61 AVEWVPYSTGQCRTTCIPYV 80
```

OM protein - protein search, using sw model

```
                                    GenCore version 5.1.6
                                    Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:             April 29, 2004, 10:50:09 ; Search time 42 Seconds
                                              (without alignments)
                                              534.580 Million cell updates/sec

Title:              US-09-856-840C-2
Perfect score:      473
Sequence:           1 MFLLVFLCCLHLVISSHTPD.........VEWVPYSTGQCRTTCIPTVG 81

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters:    1138120

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :          Published Applications AA:*
                    1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                    2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                    3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                    4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                    5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                    6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                    7: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                    8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                    9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                   10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                   11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                   12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                   13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                   14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                   15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                   16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                   17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                   18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

SUMMARIES

```
Result                Query
No.    Score    Match  Length   DB   ID         Description
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM protein - protein search, using sw model

Run on:        April 29, 2004, 10:46:48 ; Search time 20 Seconds
                                          (without alignments)
                                          389.576 Million cell updates/sec

Title:         US-09-856-840C-2
Perfect score: 473
Sequence:      1 MFLLVFLCCLHLVISSHTPD.........VEWVPYSTGQCRTTCIPTVG 81

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:        283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      PIR.78:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 77 | 16.3 | 572 | 2 | T29880 | hypothetical prote |
| 2 | 72 | 15.2 | 335 | 2 | T31559 | hypothetical prote |
| 3 | 72 | 15.2 | 1106 | 2 | T44598 | hypothetical prote |
| 4 | 71.5 | 15.1 | 407 | 2 | S44909 | 2K686.4 protein - |
| 5 | 71 | 15.0 | 1106 | 2 | T13938 | gene shuttle craft |
| 6 | 70 | 14.8 | 335 | 2 | T31560 | hypothetical prote |
| 7 | 70 | 14.8 | 335 | 2 | T31561 | hypothetical prote |
| 8 | 70 | 14.8 | 348 | 2 | S09273 | Ig alpha chain C r |
| 9 | 68.5 | 14.5 | 4660 | 2 | T42737 | gp330 protein prec |
| 10 | 68 | 14.4 | 345 | 2 | T25138 | hypothetical prote |
| 11 | 68 | 14.4 | 358 | 2 | T25137 | hypothetical prote |
| 12 | 68 | 14.4 | 417 | 2 | A54416 | prostacyclin recep |
| 13 | 68 | 14.4 | 813 | 2 | T21192 | hypothetical prote |

| No. | Score | % | Length | DB | ID | Sequence |
|---|---|---|---|---|---|---|
| 1 | 75.5 | 16.0 | 355 | 9 | US-09-948-018-2 | Sequence 2, Appli |
| 2 | 75.5 | 16.0 | 380 | 9 | US-09-948-018-36 | Sequence 36, Appl |
| 3 | 75 | 15.9 | 294 | 12 | US-10-343-650A-54 | Sequence 54, Appl |
| 4 | 74.5 | 15.8 | 136 | 9 | US-09-948-018-6 | Sequence 6, Appli |
| 5 | 73.5 | 15.5 | 485 | 14 | US-10-184-644-185 | Sequence 185, App |
| 6 | 73.5 | 15.5 | 485 | 14 | US-10-184-634-185 | Sequence 185, App |
| 7 | 73.5 | 15.5 | 485 | 14 | US-10-063-685-43 | Sequence 43, Appl |
| 8 | 71.5 | 15.1 | 56 | 9 | US-09-864-761-46095 | Sequence 46095, A |
| 9 | 71.5 | 15.1 | 85 | 9 | US-09-948-018-4 | Sequence 4, Appli |
| 10 | 71 | 15.0 | 19725 | 15 | US-10-084-846A-4 | Sequence 4, Appli |
| 11 | 68.5 | 14.5 | 4660 | 16 | US-10-464-368-74 | Sequence 74, Appl |
| 12 | 68.5 | 14.5 | 19695 | 15 | US-10-084-846A-3 | Sequence 3, Appli |
| 13 | 68 | 14.4 | 455 | 12 | US-10-424-599-221866 | Sequence 221866, |
| 14 | 68 | 14.4 | 934 | 12 | US-10-275-107-53 | Sequence 53, Appl |
| 15 | 67.5 | 14.3 | 548 | 15 | US-10-017-161-2152 | Sequence 2152, Ap |
| 16 | 67.5 | 14.3 | 548 | 15 | US-10-292-798-1798 | Sequence 1798, Ap |
| 17 | 67.5 | 14.3 | 1955 | 12 | US-10-072-012-793 | Sequence 793, App |
| 18 | 67.5 | 14.3 | 2321 | 14 | US-10-356-625-2 | Sequence 2, Appli |
| 19 | 67 | 14.2 | 202 | 9 | US-09-729-835-90 | Sequence 90, Appl |
| 20 | 67 | 14.2 | 202 | 16 | US-10-373-809-90 | Sequence 90, Appl |
| 21 | 67 | 14.2 | 227 | 14 | US-10-112-267-15 | Sequence 15, Appl |
| 22 | 67 | 14.2 | 228 | 14 | US-10-112-267-77 | Sequence 77, Appl |
| 23 | 67 | 14.2 | 229 | 14 | US-10-112-267-76 | Sequence 76, Appl |
| 24 | 67 | 14.2 | 230 | 14 | US-10-112-267-75 | Sequence 75, Appl |
| 25 | 67 | 14.2 | 231 | 14 | US-10-112-267-74 | Sequence 74, Appl |
| 26 | 67 | 14.2 | 232 | 14 | US-10-112-267-73 | Sequence 73, Appl |
| 27 | 67 | 14.2 | 233 | 14 | US-10-112-267-72 | Sequence 72, Appl |
| 28 | 67 | 14.2 | 234 | 14 | US-10-112-267-71 | Sequence 71, Appl |
| 29 | 67 | 14.2 | 235 | 14 | US-10-112-267-70 | Sequence 70, Appl |
| 30 | 67 | 14.2 | 236 | 14 | US-10-112-267-69 | Sequence 69, Appl |
| 31 | 67 | 14.2 | 237 | 14 | US-10-112-267-68 | Sequence 68, Appl |
| 32 | 67 | 14.2 | 238 | 14 | US-10-112-267-67 | Sequence 67, Appl |
| 33 | 67 | 14.2 | 239 | 14 | US-10-112-267-66 | Sequence 66, Appl |
| 34 | 67 | 14.2 | 240 | 14 | US-10-112-267-65 | Sequence 65, Appl |
| 35 | 67 | 14.2 | 241 | 14 | US-10-112-267-64 | Sequence 64, Appl |
| 36 | 67 | 14.2 | 242 | 14 | US-10-112-267-63 | Sequence 63, Appl |
| 37 | 67 | 14.2 | 243 | 14 | US-10-112-267-62 | Sequence 62, Appl |
| 38 | 67 | 14.2 | 244 | 14 | US-10-112-267-61 | Sequence 61, Appl |
| 39 | 67 | 14.2 | 245 | 14 | US-10-112-267-60 | Sequence 60, Appl |
| 40 | 67 | 14.2 | 246 | 14 | US-10-112-267-59 | Sequence 59, Appl |
| 41 | 67 | 14.2 | 247 | 14 | US-10-112-267-58 | Sequence 58, Appl |
| 42 | 67 | 14.2 | 248 | 14 | US-10-112-267-57 | Sequence 57, Appl |
| 43 | 67 | 14.2 | 249 | 14 | US-10-112-267-56 | Sequence 56, Appl |
| 44 | 67 | 14.2 | 250 | 9 | US-09-915-582-53 | Sequence 53, Appl |
| 45 | 67 | 14.2 | 250 | 9 | US-09-915-582-69 | Sequence 69, Appl |

Search completed: April 29, 2004, 10:55:50
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2004, 10:43:18 ; Search time 14 Seconds
(without alignments)
301.263 Million cell updates/sec

Title: US-09-856-840C-2
Perfect score: 473
Sequence: 1 MFILVFLCCLIHLVISSHTPD.............VEWVPYSTGQCRTTCIPTVG 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Match Length | DB | ID | Description |
| --- | --- | --- | --- | --- | --- | --- |
| 1 | 453 | 95.8 | 81 | 1 | MCP1_HIRME | P81511 hirudo medi |
| 2 | 72 | 15.2 | 603 | 1 | CFAI_MOUSE | Q61129 mus musculu |
| 3 | 71.5 | 15.1 | 407 | 1 | YO14_CAEEL | P34670 caenorhabdi |
| 4 | 71 | 15.0 | 1106 | 1 | STC_DROME | P40798 drosophila |
| 5 | 68.5 | 14.5 | 4660 | 1 | LRP2_RAT | P98158 rattus norv |
| 6 | 68 | 14.4 | 159 | 1 | KR93_HUMAN | Q9byc3 homo sapien |
| 7 | 68 | 14.4 | 288 | 1 | SPY3_HUMAN | O43610 homo sapien |
| 8 | 68 | 14.4 | 415 | 1 | P12R_MOUSE | P43252 mus musculu |
| 9 | 68 | 14.4 | 441 | 1 | YK17_SCHPO | Q9hdy3 schizosacch |
| 10 | 68 | 14.4 | 813 | 1 | YTQJ_CAEEL | Q19673 caenorhabdi |
| 11 | 68 | 14.4 | 1964 | 1 | NTC4_MOUSE | P31695 mus musculu |
| 12 | 68 | 14.4 | 3175 | 1 | RPOA_EAV | P19811 equine arte |
| 13 | 67.5 | 14.3 | 1955 | 1 | AGRI_CHICK | P31696 gallus gall |
| 14 | 67.5 | 14.3 | 2321 | 1 | NTC3_HUMAN | Q9un47 homo sapien |
| 15 | 67 | 14.2 | 250 | 1 | WSP2_HUMAN | O76076 homo sapien |
| 16 | 66.5 | 14.1 | 159 | 1 | KR98_HUMAN | Q9byq0 homo sapien |
| 17 | 66.5 | 14.1 | 1210 | 1 | AT19_MOUSE | P59509 mus musculu |

| No. | Score | % | Match Length | DB | ID | Description |
| --- | --- | --- | --- | --- | --- | --- |
| 14 | 68 | 14.4 | 1964 | 2 | T09059 | notch4 - mouse |
| 15 | 68 | 14.4 | 3175 | 1 | RRWVEV | genome polyprotein |
| 16 | 67.5 | 14.3 | 869 | 1 | JC4858 | VLDL receptor prec |
| 17 | 67.5 | 14.3 | 1955 | 2 | AGCH | agrin precursor - |
| 18 | 67.5 | 14.3 | 2321 | 2 | S78549 | notch3 protein - h |
| 19 | 67 | 14.2 | 211 | 2 | B89716 | protein F45B8.3 [i |
| 20 | 67 | 14.2 | 241 | 2 | T22216 | hypothetical prote |
| 21 | 67 | 14.2 | 400 | 2 | S35528 | surface antigen - |
| 22 | 67 | 14.2 | 548 | 1 | T25401 | hypothetical prote |
| 23 | 66.5 | 14.1 | 1959 | 1 | AGRT | agrin - rat |
| 24 | 65 | 13.7 | 435 | 2 | AD1955 | two-component sens |
| 25 | 65 | 13.7 | 498 | 1 | A48203 | interleukin-14 pre |
| 26 | 65 | 13.7 | 854 | 1 | QRHYLD | LDL receptor precu |
| 27 | 65 | 13.7 | 1945 | 2 | T13937 | plexin A - fruit f |
| 28 | 65 | 13.7 | 2643 | 1 | T29149 | hypothetical prote |
| 29 | 64.5 | 13.6 | 158 | 1 | T07597 | proteinase inhibit |
| 30 | 64 | 13.5 | 103 | 1 | TISYC2 | proteinase inhibit |
| 31 | 64 | 13.5 | 388 | 1 | A88949 | protein R09B5.5 [i |
| 32 | 64 | 13.5 | 444 | 1 | E83802 | hypothetical prote |
| 33 | 63.5 | 13.4 | 153 | 1 | XKPDC1 | proteinase inhibit |
| 34 | 63.5 | 13.4 | 226 | 2 | JQ2070 | surface antigen - |
| 35 | 63.5 | 13.4 | 972 | 2 | A30363 | glycoprotein GP330 |
| 36 | 63.5 | 13.4 | 1063 | 1 | GNWVRA | structural polypro |
| 37 | 63.5 | 13.4 | 1319 | 2 | S4995I | SSM4 protein - yea |
| 38 | 63.5 | 13.4 | 2533 | 2 | T28675 | alpha-51D immobili |
| 39 | 63.5 | 13.4 | 2533 | 2 | T28674 | alpha-51D-immobili |
| 40 | 63.5 | 13.4 | 2555 | 2 | A40043 | notch protein homo |
| 41 | 63.5 | 13.4 | 4545 | 1 | S25511 | alpha-2-macroglobu |
| 42 | 63 | 13.3 | 120 | 2 | A48837 | subgroup A Rous sa |
| 43 | 63 | 13.3 | 124 | 1 | TIBHB | trypsin inhibitor |
| 44 | 63 | 13.3 | 157 | 2 | B48837 | subgroup A Rous sa |
| 45 | 63 | 13.3 | 309 | 2 | B87576 | hypothetical prote |

Search completed: April 29, 2004, 10:50:36
Job time : 21 secs

| 18 | 66.5 | 14.1 | 1959 | 1 | AGRI_RAT | P25304 | rattus norv |
|----|------|------|------|---|----------|--------|-------------|
| 19 | 65.5 | 13.8 | 630  | 1 | ATS4_RAT | Q9esp7 | rattus norv |
| 20 | 65.5 | 13.8 | 864  | 1 | AD15_MOUSE | O88839 | mus musculu |
| 21 | 65   | 13.7 | 604  | 1 | CPAI_RAT | Q9wuw3 | rattus norv |
| 22 | 65   | 13.7 | 854  | 1 | LDLR_CRIGR | P35950 | cricetulus |
| 23 | 64.5 | 13.6 | 158  | 1 | IP2X_SOLTU | Q00782 | solanum tub |
| 24 | 64   | 13.5 | 154  | 1 | IP2X_SOLTU | Q41488 | solanum tub |
| 25 | 64   | 13.5 | 616  | 1 | TRI1_HUMAN | Q9y6q6 | homo sapien |
| 26 | 64   | 13.5 | 1696 | 1 | PCK5_BRACL | Q9njl5 | branchiosto |
| 27 | 63.5 | 13.4 | 153  | 1 | IP2X_SOLTU | P01080 | solanum tub |
| 28 | 63.5 | 13.4 | 1063 | 1 | POL5_RUBVR | P19725 | rubella vir |
| 29 | 63.5 | 13.4 | 1319 | 1 | SSM4_YEAST | P40018 | saccharomyc |
| 30 | 63.5 | 13.4 | 2556 | 1 | NTC1_HUMAN | P46531 | homo sapien |
| 31 | 63   | 13.3 | 124  | 1 | IBB_HORVU | P12940 | hordeum vul |
| 32 | 63   | 13.3 | 157  | 1 | RSVR_COTJA | P98162 | coturnix co |
| 33 | 63   | 13.3 | 286  | 1 | HXBD_MOUSE | P70321 | mus musculu |
| 34 | 63   | 13.3 | 2531 | 1 | NTC1_MOUSE | Q01705 | mus musculu |
| 35 | 63   | 13.3 | 2531 | 1 | NTC1_RAT | O07008 | rattus norv |
| 36 | 62.5 | 13.2 | 176  | 1 | TR23_MOUSE | Q9ez63 | mus musculu |
| 37 | 62.5 | 13.2 | 291  | 1 | US02_HSV2H | P13222 | herpes simp |
| 38 | 62.5 | 13.2 | 416  | 1 | PROA_THETH | P54903 | thermus the |
| 39 | 62.5 | 13.2 | 2524 | 1 | NOTC_XENLA | P21783 | xenopus lae |
| 40 | 62   | 13.1 | 1223 | 1 | AT14_HUMAN | Q8wx88 | homo sapien |
| 41 | 62   | 13.1 | 2193 | 1 | POLG_CX16G | Q65900 | c genome po |
| 42 | 61.5 | 13.0 | 285  | 1 | VIE1_HSVB4 | P27426 | bovine herp |
| 43 | 61.5 | 13.0 | 1063 | 1 | POL5_RUBVT | P07566 | rubella vir |
| 44 | 61   | 12.9 | 292  | 1 | NADA_METKA | Q8tze6 | methanopyru |
| 45 | 60.5 | 12.8 | 127  | 1 | K410_HUMAN | Q9byq7 | homo sapien |

RESULT 1
```
ID   MCPI_HIRME     STANDARD;      PRT;    81 AA.
AC   P81511;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Metallocarboxypeptidase inhibitor precursor (LCI).
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 16-81.
RX   MEDLINE=99047680; PubMed=9830043;
RA   Reverter D., Vendrell J., Canals F., Horstmann J., Aviles F.X.,
RA   Fritz H., Sommerhoff C.P.;
RT   "A carboxypeptidase inhibitor from the medical leech Hirudo
RT   medicinalis. Isolation, sequence analysis, cDNA cloning, recombinant
RT   expression, and characterization.";
RL   J. Biol. Chem. 273:32927-32933(1998).
CC   -!- FUNCTION: tightly binding, competitive inhibitor of different
CC       types of pancreatic-like carboxypeptidases.
CC   -!- PTM: The cysteine residues are involved in intrachain disulfide
CC       bonds.
CC   -!- MASS SPECTROMETRY: MW=7326; METHOD=MALDI; RANGE=16-81.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AJ010948; CAA09422.1; -.
DR   PDB; 1DTD; 12-JUL-00; -.
DR   PDB; 1DTV; 19-JUL-00.
KW   Metalloenzyme inhibitor; Signal; 3D-structure.
FT   SIGNAL        1     15
FT   CHAIN        16     81       METALLOCARBOXYPEPTIDASE INHIBITOR.
FT   ACT_SITE     80     80       INTERACTION WITH CARBOXYPEPTIDASE (BY
FT                                SIMILARITY).
SQ   SEQUENCE   81 AA;  9068 MW;  7D7E175E6933322A CRC64;
```

ALIGNMENTS

```
Query Match             95.8%;  Score 453;  DB 1;  Length 81;
Best Local Similarity   97.5%;  Pred. No. 6.4e-41;
Matches   78;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         1 MFLLVFLCCLHLVISSHTPDESFLCTQPPDQVCCFICRGAAPLPSEGECNPHPTAPWCREG 60
             ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         1 MFLLVFLCCLHLVISSHTPDESFLCXQPPDQVCCFICRGAAPLPSEGECNPHPTAPWCREG 60

Qy        61 AVEWVPYSTGQCRTTCIPTV 80
             |||||||||||||||||| |
Db        61 AVEWVPYSTGQCRTTCIPYV 80
```

Search completed: April 29, 2004, 10:49:12
Job time : 16 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:          April 29, 2004, 10:46:18 ; Search time 39 Seconds
                 (without alignments)
                 655.307 Million cell updates/sec

Title:           US-09-856-840C-2
Perfect score:   473
Sequence:        1 MFILVFLCLLHLVISHTPD.........VEWVPYSTGQCRTTCIPTVG 81

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched:        1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:     1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :
     SPTREMBL_25:*
     1: sp_archea:*
     2: sp_bacteria:*
     3: sp_fungi:*
     4: sp_human:*
     5: sp_invertebrate:*
     6: sp_mammal:*
     7: sp_mhc:*
     8: sp_organelle:*
     9: sp_phage:*
    10: sp_plant:*
    11: sp_rodent:*
    12: sp_virus:*
    13: sp_vertebrate:*
    14: sp_unclassified:*
    15: sp_rvirus:*
    16: sp_bacteriap:*
    17: sp_archeap:*

                              SUMMARIES

Result
No.   Score   Query   Match Length   DB   ID   Description
-------------------------------------------------------------

| No. | Score | | Match Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 81 | 17.1 | 340 | 5 | P90627 | leishmania |
| 2 | 80 | 16.9 | 421 | 5 | Q86JD6 | dictyostelli |
| 3 | 77 | 16.3 | 572 | 5 | Q19594 | caenorhabdi |
| 4 | 75.5 | 16.0 | 355 | 4 | Q9H665 | homo sapien |
| 5 | 75.5 | 16.0 | 821 | 5 | Q22631 | caenorhabdi |
| 6 | 74 | 15.6 | 340 | 5 | Q8WT30 | leishmania |
| 7 | 74 | 15.6 | 340 | 5 | Q9GQM5 | leishmania |
| 8 | 72 | 15.2 | 340 | 5 | Q9GQN7 | leishmania |
| 9 | 72 | 15.2 | 335 | 5 | Q9N6L3 | caenorhabdi |
| 10 | 72 | 15.2 | 1099 | 5 | Q9Y025 | drosophila |
| 11 | 71.5 | 15.1 | 1106 | 5 | Q8IP49 | drosophila |
| 12 | 71 | 15.0 | 340 | 5 | Q25519 | leishmania |
| 13 | 71 | 15.0 | 451 | 5 | Q86KC7 | dictyostelli |
| 14 | 71 | 15.0 | 1069 | 5 | Q9VBN2 | drosophila |
| 15 | 70 | 14.8 | 335 | 5 | Q9NF69 | caenorhabdi |
| 16 | 70 | 14.8 | 335 | 5 | Q9NF70 | caenorhabdi |
| 17 | 70 | 14.8 | 419 | 5 | Q9NA38 | caenorhabdi |
| 18 | 70 | 14.8 | 420 | 5 | Q9NA61 | caenorhabdi |
| 19 | 69 | 14.6 | 218 | 5 | Q19618 | caenorhabdi |
| 20 | 68.5 | 14.5 | 502 | 16 | Q7UE37 | rhodopirell |
| 21 | 68.5 | 14.5 | 765 | 5 | Q9NL50 | sarcophaga |
| 22 | 68 | 14.4 | 159 | 4 | Q9BXQ3 | homo sapien |
| 23 | 68 | 14.4 | 212 | 11 | Q8CC99 | mus musculu |
| 24 | 68 | 14.4 | 358 | 5 | Q9U362 | caenorhabdi |
| 25 | 68 | 14.4 | 3175 | 12 | Q91DM2 | equine arte |
| 26 | 67.5 | 14.3 | 325 | 10 | Q8LG72 | arabidopsis |
| 27 | 67.5 | 14.3 | 869 | 13 | 042126 | xenopus lae |
| 28 | 67.5 | 14.3 | 4007 | 4 | Q86XX4 | homo sapien |
| 29 | 67 | 14.2 | 241 | 5 | 045522 | caenorhabdi |
| 30 | 67 | 14.2 | 355 | 13 | Q802V2 | brachydanio |
| 31 | 67 | 14.2 | 400 | 12 | Q81108 | hepatitis b |
| 32 | 67 | 14.2 | 527 | 5 | P91835 | caenorhabdi |
| 33 | 67 | 14.2 | 649 | 6 | Q28657 | oryctolagus |
| 34 | 66.5 | 14.1 | 159 | 4 | Q9BYQ0 | homo sapien |
| 35 | 66.5 | 14.1 | 769 | 5 | Q8MRL5 | drosophila |
| 36 | 66.5 | 14.1 | 1059 | 5 | Q9W493 | drosophila |
| 37 | 66.5 | 14.1 | 1149 | 4 | Q13577 | homo sapien |
| 38 | 66.5 | 14.1 | 2026 | 4 | O00468 | homo sapien |
| 39 | 66 | 14.0 | 847 | 13 | Q90WI2 | oncorhynchu |
| 40 | 66 | 14.0 | 1064 | 5 | Q7YU01 | drosophila |
| 41 | 65.5 | 13.8 | 324 | 10 | Q9SM86 | oryza sativ |
| 42 | 65.5 | 13.8 | 651 | 4 | Q86UZ4 | homo sapien |
| 43 | 65.5 | 13.8 | 809 | 11 | Q8CA82 | mus musculu |
| 44 | 65.5 | 13.8 | 833 | 11 | Q8K384 | mus musculu |
| 45 | 65.5 | 13.8 | 845 | 11 | Q8BNJ2 | mus musculu |

P90627 leishmania
Q86jd6 dictyosteli
Q19594 caenorhabdi
Q9H665 homo sapien
Q22631 caenorhabdi
Q8wt30 leishmania
Q9GQM5 leishmania
Q9GQN7 leishmania
Q9N6L3 caenorhabdi
Q9Y025 drosophila
Q8IP49 drosophila
Q25519 leishmania
Q86KC7 dictyosteli
Q9VBN2 drosophila
Q9NF69 caenorhabdi
Q9NF70 caenorhabdi
Q9NA38 caenorhabdi
Q9NA61 caenorhabdi
Q19618 caenorhabdi
Q7UE37 rhodopirell
Q9NL50 sarcophaga
Q9BXQ3 homo sapien
Q8CC99 mus musculu
Q9U362 caenorhabdi
Q91DM2 equine arte
Q8LG72 arabidopsis
042126 xenopus lae
Q86XX4 homo sapien
045522 caenorhabdi
Q802V2 brachydanio
Q81108 hepatitis b
P91835 caenorhabdi
Q28657 oryctolagus
Q9BYQ0 homo sapien
Q8MRL5 drosophila
Q9W493 drosophila
Q13577 homo sapien
000468 homo sapien
Q90WI2 oncorhynchu
Q7YU01 drosophila
Q9SM86 oryza sativ
Q86UZ4 homo sapien
Q8CA82 mus musculu
Q8K384 mus musculu
Q8BNJ2 mus musculu

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Search completed: April 29, 2004, 10:50:04
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 06:56:35 ; Search time 2007 Seconds
(without alignments)
10042.108 Million cell updates/sec

Title:          US-09-856-840C-1
Perfect score:  465
Sequence:       1 gacttggtaacttcattcgat.........taaaaaaaaagaaaaaaaa 465

Scoring table:  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:  3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters:          6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :  GenEmbl:*

```
 1: gb_ba:*           28: em_un:*
 2: gb_htg:*          29: em_vi:*
 3: gb_in:*           30: em_htg_hum:*
 4: gb_om:*           31: em_htg_inv:*
 5: gb_ov:*           32: em_htg_other:*
 6: gb_pat:*          33: em_htg_mus:*
 7: gb_ph:*           34: em_htg_pln:*
 8: gb_pl:*           35: em_htg_rod:*
 9: gb_pr:*           36: em_htg_mam:*
10: gb_ro:*           37: em_htg_vrt:*
11: gb_sts:*          38: em_sy:*
12: gb_sy:*           39: em_htgo_hum:*
13: gb_un:*           40: em_htgo_mus:*
14: gb_vi:*           41: em_htgo_other:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| C | Result No. | Score | % Match | Query Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 465 | 100.0 | 465 | 6 | HME010948 | AJ010948 Hirudo me |
| | 2 | 465 | 100.0 | 465 | 6 | AX026084 | AX026084 Sequence |
| | 3 | 50.2 | 10.8 | 110000 | 2 | AC116305_1 | AX026084 Continuation (2 of |
| | 4 | 49.8 | 10.7 | 182870 | 3 | AC116960 | AC116960 Dictyoste |
| | 5 | 49.2 | 10.6 | 6424 | 3 | AC116924 | AC116924 Dictyoste |
| c | 6 | 49.2 | 10.6 | 110000 | 2 | PFMAL13_17 | PFMAL13_17 Continuation (18 o |
| | 7 | 48.4 | 10.4 | 13138 | 3 | AC116305_4 | AC116305_4 Continuation (5 of |
| | 8 | 48.4 | 10.4 | 110000 | 2 | PFMAL8P1_01 | PFMAL8P1_01 Continuation (2 of |
| | 9 | 48.4 | 10.4 | 110000 | 3 | AC116305_3 | AC116305_3 Continuation (4 of |
| | 10 | 48.4 | 10.4 | 302156 | 3 | AC116977 | AC116977 Dictyoste |
| | 11 | 48 | 10.3 | 110000 | 2 | PFMAL6P1_12 | PFMAL6P1_12 Continuation (13 o |
| | 12 | 47.6 | 10.2 | 3016 | 3 | DDU31631 | U31631 Dictyosteli |
| | 13 | 47.6 | 10.2 | 169546 | 2 | AC004157 | AC004157 Plasmodi |
| c | 14 | 47.6 | 10.2 | 250707 | 3 | AE014848 | AE014848 Plasmodi |
| | 15 | 47.6 | 10.2 | 349954 | 6 | AX196297 | AX196297 Sequence |
| | 16 | 47.4 | 10.2 | 2523 | 9 | BC038509 | BC038509 Homo sapi |
| | 17 | 47.4 | 10.2 | 132254 | 3 | AC116330 | AC116330 Dictyoste |
| | 18 | 47.2 | 10.2 | 2917 | 9 | BC054514 | BC054514 Homo sapi |
| c | 19 | 47.2 | 10.2 | 110000 | 3 | AC116957_0 | AC116957 Dictyoste |
| | 20 | 47.2 | 10.2 | 257109 | 3 | AC115577 | AC115577 Dictyoste |
| | 21 | 47 | 10.1 | 27694 | 8 | HASMT | D31785 Pichia cana |
| c | 22 | 47 | 10.1 | 125623 | 3 | AC115599 | AC115599 Dictyoste |
| | 23 | 46.8 | 10.1 | 57203 | 3 | AC116989 | AC116989 Dictyoste |
| | 24 | 46.6 | 10.0 | 31343 | 2 | AC115576 | AC115576 Dictyoste |
| | 25 | 46.6 | 10.0 | 31712 | 8 | AP000415 | AP000415 Arabidops |
| c | 26 | 46.6 | 10.0 | 33270 | 3 | AC116921 | AC116921 Dictyoste |
| c | 27 | 46.6 | 10.0 | 110000 | 2 | PFMAL7P1_08 | PFMAL7P1_08 Continuation (9 of |
| c | 28 | 46.6 | 10.0 | 117113 | 8 | AC146575 | AC146575 Medicago |
| c | 29 | 46.6 | 10.0 | 234081 | 3 | PFMAL4P2 | PFMAL4P2 Plasmodiu |
| c | 30 | 46.6 | 10.0 | 254733 | 3 | AC117075 | AC117075 Plasmodiu |
| c | 31 | 46.6 | 10.0 | 254709 | 3 | AC115577 | AC115577 Dictyoste |
| c | 32 | 46.4 | 10.0 | 154071 | 3 | AC115598 | AC115598 Dictyoste |
| c | 33 | 46.4 | 10.0 | 250195 | 3 | AE014831 | AE014831 Plasmodiu |

| 34 | 46.4 | 10.0 | 251551 | 3 | AE014844 | AE014844 Plasmodiu |
|----|------|------|--------|---|----------|--------------------|
| 35 | 46.4 | 10.0 | 254449 | 3 | AE014817 | AE014817 Plasmodiu |
| 36 | 46.2 | 9.9 | 286 | 3 | DDIACT21 | J01267 Dictyosteli |
| 37 | 46.2 | 9.9 | 286 | 18 | DDACT3 | V00184 Slime mold |
| 38 | 46.2 | 9.9 | 1976 | 9 | BC025253 | BC025253 Homo sapi |
| 39 | 46.2 | 9.9 | 2177 | 5 | BC063356 | BC063356 Silurana |
| 40 | 46.2 | 9.9 | 250029 | 3 | AE014839 | AE014839 Plasmodiu |
| 41 | 46.2 | 9.9 | 266544 | 3 | AC116956 | AC116956 Dictyoste |
| 42 | 46 | 9.9 | 4325 | 10 | BC060196 | BC060196 Mus muscu |
| 43 | 46 | 9.9 | 40880 | 8 | SPCC1235 | AL031764 S.pombe c |
| 44 | 46 | 9.9 | 64394 | 9 | AL928596 | AL928596 Human DNA |
| 45 | 45.8 | 9.8 | 6694 | 9 | HSM808397 | BX648249 Homo sapi |

ALIGNMENTS

RESULT 1

```
LOCUS       HME010948              465 bp    mRNA    linear   INV 02-DEC-1998
DEFINITION  Hirudo medicinalis mRNA for metallocarboxypeptidase inhibitor.
ACCESSION   AJ010948
VERSION     AJ010948.1  GI:3954832
KEYWORDS    metallocarboxypeptidase inhibitor.
SOURCE      Hirudo medicinalis (medicinal leech)
  ORGANISM  Hirudo medicinalis
            Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
            Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
REFERENCE   1
  AUTHORS   Reverter,D., Vendrell,J., Canals,F., Horstmann,J., Aviles,F.X.,
            Fritz,H. and Sommerhoff,C.P.
  TITLE     A carboxypeptidase inhibitor from the medical leech Hirudo
            medicinalis. Isolation, sequence analysis, cDNA cloning,
            recombinant expression, and characterization
  JOURNAL   J. Biol. Chem. 273 (49), 32927-32933 (1998)
  MEDLINE   99047680
   PUBMED   9830043
REFERENCE   2  (bases 1 to 465)
  AUTHORS   Aviles,F.X.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-1998) Aviles F.X., Institut de Biologia
            Fonamental, Universitat Autonoma de Barcelona, Bellaterra, 08193,
            SPAIN
FEATURES             Location/Qualifiers
     source          1..465
                     /organism="Hirudo medicinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:6421"
     CDS             22..267
                     /codon_start=1
                     /evidence=experimental
                     /product="metallocarboxypeptidase inhibitor"
                     /protein_id="CAA09422.1"
                     /db_xref="GI:3954833"
                     /db_xref="GOA:P81511"
                     /db_xref="SWISS-PROT:P81511"
                     /translation="MFLLVFLCLIHLVISSHTPDESFLCYQPDQVCCFICRGAAPLPS
                     EGECNPHPTAPWCREGAVEWPYSTGQCRTICIPYVE"
     sig_peptide     22..66
     mat_peptide     67..264
     polyA_signal    426..431
                     /product="metallocarboxypeptidase inhibitor"
ORIGIN
```

Query Match 100.0%; Score 465; DB 3; Length 465;
Best Local Similarity 100.0%; 
Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GACTTGGTAACTCATTCGATCATCATGTTTTCTTGCTTGTTTTTCTGCTTGTTTTTCTGCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GACTTGGTAACTCATTCGATCATCATGTTTTCTTGCTTGTTTTTCTGCTTGTTTTTCTGCT 60

Qy     61 ATTTCGTCGCATACCACCAGATGAGAGTTTCTTGTGCTACCAGACCAGGTGTGCTGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATTTCGTCGCATACCACCAGATGAGAGTTTCTTGTGCTACCAGACCAGGTGTGCTGT 120

Qy    121 TTCATTTGCAGAGGAGGGGCACCTTTCGCCTTCAGAAGGGAATCACATCCTACA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTCATTTGCAGAGGAGGGGCACCTTTCGCCTTCAGAAGGGAATCACATCCTACA 180

Qy    181 GCACCCTGGTGCCGGGAAGGGGCGTGTGAGATGGGTCCCCTACTCTACTGTCAATGTGCGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCACCCTGGTGCCGGGAAGGGGCGTGTGAGATGGGTCCCCTACTCTACTGTCAATGTGCGC 240

Qy    241 ACAACCTGCATCCCATATGTCGAGTAGATGACCCATCGTGTGTGTCACTGATGCGAGGCTAA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACAACCTGCATCCCATATGTCGAGTAGATGACCCATCGTGTGTGTCACTGATGCGAGGCTAA 300

Qy    301 CTCTCATTATTTCCTGAACGCGATCCTTGTTGAAAATTAAGGGCATTTCTTCTTGACT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTCTCATTATTTCCTGAACGCGATCCTTGTTGAAAATTAAGGGCATTTCTTCTTGACT 360

Qy    361 AATTATTTTGCTGAGTTAAAATAATAAAATAATTGAAGCATTATTTAATAATGTTCTC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AATTATTTTGCTGAGTTAAAATAATAAAATAATTGAAGCATTATTTAATAATGTTCTC 420

Qy    421 GTTTGAATAAAAATATGATCCGAAAGATAAAAAAAAAAGAAAAAAA 465
          |||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTTTGAATAAAAATATGATCCGAAAGATAAAAAAAAAAGAAAAAAA 465
```

RESULT 2

```
LOCUS       AX026084               465 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 1 from Patent WO0031140.
ACCESSION   AX026084
VERSION     AX026084.1  GI:10187517
KEYWORDS    .
SOURCE      Hirudo medicinalis (medicinal leech)
  ORGANISM  Hirudo medicinalis
            Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
            Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
REFERENCE   1
  AUTHORS   Fritz,H., Horstmann,J., Sommerhoff,C.P., Aviles,F.X., Canals,F.,
```

TITLE      Querol,E., Reverter,D. and Vendrell,J.
           Inhibitor of metalocarboxypeptidases as fibrinolytic agent
JOURNAL     Patent: WO 0031140-A 1 02-JUN-2000;
           FRITZ HANS (DE) ; HORSTMANN JEANNY (DE) ; LUDWIG MAXIMILIANS UNI
           MUENCHE (DE) ; SOMMERHOFF CHRISTIAN P (DE) ; AVILES FRANCESC X (ES)
           ; UNIV BARCELONA AUTONOMA (ES) ; CANALS FRANCESC (ES) ; QUEROL
           ENRIQUE (ES) ; REVERTER DAVID (ES) ; VENDRELL JOSEP (ES)

FEATURES             Location/Qualifiers
     source          1..465
                     /organism="Hirudo medicinalis"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:6421"
     CDS             22..267
                     /note="unnamed protein product; Product=LCI"
                     /codon_start=1
                     /protein_id="CAC09071.1"
                     /db_xref="GI:10187518"
                     /db_xref="REMTREMBL:CAC09071"
                     /translation="MFLLVFLCCLHLVISSHTPDESFLCXQPDQVCCFICRGAAPLPS
                     EGICNPHPTAPWCREGAVEWPYSTGQCRTICIPYVE"

ORIGIN

Query Match         100.0%;   Score 465;  DB 6;   Length 465;
Best Local Similarity  100.0%;   Pred. No. 9.9e-95;
Matches  465; Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1 GACTTGGTAACTCAATTCGATTCATGTTTCTCGCTCGTTTTTCGTTGCTGCCTCCCACCTGGGTG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GACTTGGTAACTCAATTCGATTCATGTTTCTCGCTCGTTTTTCGTTGCTGCCTCCCACCTGGTG 60

Qy      61 ATTTCGTCGCATACCACCAGATGAGAGTTTTCTTGTGTCTACCAACCAGACCAGGTGTGCTGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ATTTCGTCGCATACCACCAGATGAGAGTTTTCTTGTGTCTACCAACCAGACCAGGTGTGCTGT 120

Qy     121 TTCATTTGCRAGAGGAGCGGCGCACCTTTGCCTTCAGAAGGGAATGCAATCCACATCCTACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TTCATTTGCRAGAGGAGCGGCGCACCTTTGCCTTCAGAAGGGAATGCAATCCACATCCTACA 180

Qy     181 GCACCCTGGTGCCCGGGAAGGGGGCGTRAGAGTGGGTTCCCTACTCTACTGGTCAATGTCGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCACCCTGGTGCCCGGGAAGGGGGCGTRAGAGTGGGTTCCCTACTCTACTGGTCAATGTCGC 240

Qy     241 ACAACCTGCATCCCATATGTCGAGTAGATGACCCATCGTGTGTCATCGATCCGAGGCTAA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACAACCTGCATCCCATATGTCGAGTAGATGACCCATCGTGTGTCATCGATCCGAGGCTAA 300

Qy     301 CTCTCATTATTTTTCCTGAACGGCATCCTTGTTGTAAATTTAAGGGCCATTTCTCTTCTTGACT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTCTCATTATTTTTCCTGAACGGCATCCTTGTTGTAAATTTAAGGGCCATTTCTCTTCTTGACT 360

Qy     361 AATTAATTTTGCTGAGTTAAAATAATAAAAATAATAATTGAAGCCATTATTTAATAATGTTCTC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AATTAATTTTGCTGAGTTAAAATAATAAAAATAATAATTGAAGCCATTATTTAATAATGTTCTC 420

Qy     421 GTTTGAATAAAATATGATCGAAAGATAAAAAAAAAAAGAAAAAAA 465
           |||||||||||||||||||||||||||||||||||||||||||||
Db     421 GTTTGAATAAAATATGATCGAAAGATAAAAAAAAAAAGAAAAAAA 465

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 06:54:50 ; Search time 341 seconds
(without alignments)
5792.997 Million cell updates/sec

Title:        US-09-856-840C-1
Perfect score: 465
Sequence:     1 gactggtaactcattcgat.........taaaaaaaaaagaaaaaa 465
Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0
Searched:     3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters:   6747726
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
Database :    N_Geneseq_29Jan04:*
              1: geneseqn1980s:*
              2: geneseqn1990s:*
              3: geneseqn2000s:*
              4: geneseqn2001as:*
              5: geneseqn2001bs:*
              6: geneseqn2002s:*
              7: geneseqn2002as:*
              8: geneseqn2003bs:*
              9: geneseqn2003cs:*
             10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 465 | 100.0 | 465 | 3 | AAA11268 | Aaa11268 Hirudo me |
| 2 | 47.6 | 10.2 | 110000 | 5 | AAI61373_2 | Continuation (3 of |
| 3 | 45 | 9.7 | 266 | 5 | ABV07596 | Abv07596 Human pro |
| 4 | 45 | 9.7 | 887 | 3 | AAC59297 | Aac59297 Human sec |
| 5 | 45 | 9.7 | 6071 | 6 | ABL32367 | Abl32367 Human imm |
| 6 | 45 | 9.7 | 6071 | 6 | ABL34483 | Abl34483 Human met |
| 7 | 45 | 9.7 | 6071 | 6 | ABL70154 | Abl70154 Chemical1 |

| | No. | Score | % | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| c | 8 | 44.8 | 9.6 | 337 | 7 | ABX41811 | Abx41811 Bovine ES |
| c | 9 | 44.8 | 9.6 | 8779 | 6 | AAS61382 | Aas61382 Human gen |
| c | 10 | 44.4 | 9.5 | 370 | 5 | ABV07958 | Abv07958 Human pro |
| c | 11 | 44.4 | 9.5 | 19131 | 4 | AAS46716 | Aas46716 Tumour su |
| c | 12 | 43.8 | 9.4 | 372 | 5 | ABV37528 | Abv37528 Human pro |
| c | 13 | 43.8 | 9.4 | 5511 | 5 | ABL33871 | Abl33871 Human imm |
| c | 14 | 43.8 | 9.4 | 1110000 | 6 | ABA92787_1 | Continuation (2 of |
| c | 15 | 43.4 | 9.3 | 970 | 6 | ABQ54211 | Abq54211 Human ova |
| c | 16 | 43.4 | 9.3 | 1333 | 7 | ACA96036 | Aca96036 Trifolium |
| c | 17 | 43.2 | 9.3 | 425 | 4 | AAI92310 | Aai92310 Human pol |
| c | 18 | 43.2 | 9.3 | 3197 | 8 | ACF05254 | Acf05254 Plasmodiu |
| c | 19 | 43 | 9.2 | 40862 | 6 | ABL34072 | Abl34072 Human imm |
| c | 20 | 42.8 | 9.2 | 294 | 4 | AAH70082 | Aah70082 Human cer |
| c | 21 | 42.8 | 9.2 | 299 | 2 | AAV21217 | Aav21217 Partial n |
| c | 22 | 42.8 | 9.2 | 332 | 4 | AAH70043 | Aah70043 Human cer |
| c | 23 | 42.8 | 9.2 | 473 | 8 | ACH26237 | Ach26237 Human adu |
| c | 24 | 42.8 | 9.2 | 631 | 6 | ABQ25138 | Abq25138 Oligonucl |
| c | 25 | 42.6 | 9.2 | 631 | 5 | ABQ25139 | Abq25139 Oligonucl |
| c | 26 | 42.6 | 9.2 | 1781 | 9 | ADES8028 | Ades8028 Human gen |
| c | 27 | 42.6 | 9.2 | 1781 | 9 | ADES8032 | Ades8032 Human gen |
| c | 28 | 42.6 | 9.2 | 6731 | 9 | ABK39963 | Abk39963 Human che |
| c | 29 | 42.6 | 9.2 | 8056 | 7 | ABZ10246 | Abz10246 Haematopo |
| c | 30 | 42.4 | 9.1 | 377 | 7 | ABX42254 | Abx42254 Bovine ES |
| c | 31 | 42.4 | 9.1 | 3138 | 2 | AAQ17712 | Aaq17712 Shuttle v |
| c | 32 | 42.4 | 9.1 | 3549 | 3 | AAA70223 | Aaa70223 Plasmodiu |
| c | 33 | 42.2 | 9.1 | 423 | 7 | ABX38651 | Abx38651 Bovine ES |
| c | 34 | 42.2 | 9.1 | 464 | 4 | AAH33241 | Aah33241 Human col |
| c | 35 | 42.2 | 9.1 | 1262 | 3 | AAC79885 | Aac79885 Human sec |
| c | 36 | 42.2 | 9.1 | 1262 | 6 | ABK70506 | Abk70506 Human CDN |
| c | 37 | 42.2 | 9.1 | 10039 | 6 | ABL34042 | Abl34042 Human imm |
| c | 38 | 42.2 | 9.1 | 19124 | 2 | AAT72882 | Aat72882 Plasmodiu |
| c | 39 | 42.2 | 9.1 | 19124 | 3 | AAZ98287 | Aaz98287 Plasmodiu |
| c | 40 | 42 | 9.0 | 843 | 5 | ABV16074 | Abv16074 Human pro |
| c | 41 | 42 | 9.0 | 939 | 6 | ABK33574 | Abk33574 cDNA enco |
| c | 42 | 42 | 9.0 | 939 | 7 | ACA66879 | Aca66879 cDNA enco |
| c | 43 | 42 | 9.0 | 939 | 7 | ACD68631 | Acd68631 Novel hum |
| c | 44 | 42 | 9.0 | 939 | 7 | ACA68535 | Aca68535 Novel hum |
| c | 45 | 42 | 9.0 | 939 | 8 | ABT44264 | Abt44264 Human PRO |

ALIGNMENTS

RESULT 1
AAA11268
ID   AAA11268 standard; cDNA; 465 BP.
XX
AC   AAA11268;
XX
DT   08-NOV-2000 (first entry)
XX
DE   Hirudo medicinalis metallocarboxypeptidase inhibitor cDNA.
XX
KW   Recombinant; leech; metallocarboxypeptidase inhibitor; fibrin;
KW   plasma carboxypeptidase B; fibrinolysis inhibitor; plasminogen;
KW   blood clot; ds.
XX

OS   Hirudo medicinalis.
XX
FH   Key             Location/Qualifiers
FT   CDS             22..267
FT                   /*tag= a
FT                   /product= "metallocarboxypeptidase inhibitor"
FT   sig_peptide     22..66
FT                   /*tag= b
FT   mat_peptide     67..264
FT                   /*tag= c
XX
PN   WO200031140-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-ES000378.
XX
PR   25-NOV-1998;   98ES-0002524.
XX
PA   (UYBA-) UNIV AUTONOMA BARCELONA.
PA   (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
XX
PI   Reverter D,  Vendrell J,  Canals F,  Horstmann J,  Querol E,  Fritz H;
PI   Sommerhoff CP,  Aviles FX;
XX
DR   WPI: 2000-400047/34.
DR   P-PSDB; AAY92938.
XX
PT   New recombinant nucleic acid encoding metallocarboxypeptidase inhibitor,
PT   useful as fibrinolytic agent, is derived from the leech Hirudo
PT   medicinalis.
XX
PS   Claim 2; Page 17; 23pp; Spanish.
XX
CC   This sequence represents a recombinant nucleic acid that codes for a
CC   protein derived from Hirudo medicinalis (leeches) that inhibits
CC   metallocarboxypeptidases, particularly of plasma carboxypeptidase B which
CC   inhibits fibrinolysis by destroying the binding site, in plasminogen, for
CC   fibrin. The inhibitor is useful as a fibrinolytic agent, thus promotes
CC   activity of plasminogen and speeds up lysis of blood clots
XX
SQ   Sequence 465 BP; 129 A; 99 C; 96 G; 141 T; 0 U; 0 Other;

Query Match             100.0%;  Score 465;  DB 3;  Length 465;
Best Local Similarity   100.0%;  Pred. No. 4.6e-99;
Matches  465;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1 GACTGGTAACTCAATTCGAATCATGTTTCTTGCTCGTTTCCTGTGCTGCCTTCCACCTGGTG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GACTGGTAACTCAATTCGAATCATGTTTCTTGCTCGTTTCCTGTGCTGCCTTCCACCTGGTG 60

Qy      61 ATTTCGTCGCATACACCAGATGAGAGTTTCTTGTTGCTACCAGACCAGGTCTGCTGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ATTTCGTCGCATACACCAGATGAGAGTTTCTTGTTGCTACCAGACCAGGTCTGCTGT 120

Qy     121 TTCATTTGCAGAGGAGGCGGGCACCTTTGCCTTCAGAGGGGGAATGCAATCACATCCTACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TTCATTTGCAGAGGAGGCGGGCACCTTTGCCTTCAGAGGGGGAATGCAATCACATCCTACA 180

Qy     181 GCACCCTGGTGCCGGGAAGGGGCGTTAGAGTGGGTTCCCTACTTCTTACTGGTCAATGTCGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCACCCTGGTGCCGGGAAGGGGCGTTAGAGTGGGTTCCCTACTTCTTACTGGTCAATGTCGC 240

Qy     241 ACAACCTGCATCCCATAGTCGAGTAGATGACCCATGTGTTGCACTGATCGGAGGCTAA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACAACCTGCATCCCATAGTCGAGTAGATGACCCATGTGTTGCACTGATCGGAGGCTAA 300

Qy     301 CTCTCATTATTTCCTGAACGCCATCCTTGTTGAAATTTAAGGGCATTTCTTCTTGACT 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTCTCATTATTTCCTGAACGCCATCCTTGTTGAAATTTAAGGGCATTTCTTCTTGACT 360

Qy     361 AATTATTTTGCTGAGTTAAAATAATAAAAATAAAATTGAACCATTATTAATAATGTTCTC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AATTATTTTGCTGAGTTAAAATAATAAAAATAAAATTGAACCATTATTAATAATGTTCTC 420

Qy     421 GTTTGAATAAAATATGATCGAAAGATAAAAAAAAAAAAGAAAAAAAA 465
           ||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GTTTGAATAAAATATGATCGAAAGATAAAAAAAAAAAAGAAAAAAAA 465

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search using sw model

Run on:            April 30, 2004, 09:28:21 ; Search time 323 Seconds
                   (without alignments)
                   6512.108 Million cell updates/sec

Title:             US-09-856-840C-1
Perfect score:     465
Sequence:          1 gactggtaactcatcgat.........taaaaaaaaagaaaaaaa 465

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters:     5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:   Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Database :         Published_Applications_NA.*

1:  /cgn2_6/ptcdata/1/pubpna/US07_PUBCOMB.seq:*
2:  /cgn2_6/ptcdata/1/pubpna/PCT_NEW_PUB.seq:*
3:  /cgn2_6/ptcdata/1/pubpna/US09C_PUBCOMB.seq:*
4:  /cgn2_6/ptcdata/1/pubpna/US06_PUBCOMB.seq:*
5:  /cgn2_6/ptcdata/1/pubpna/US07_NEW_PUB.seq:*
6:  /cgn2_6/ptcdata/1/pubpna/PCTUS_PUBCOMB.seq:*
7:  /cgn2_6/ptcdata/1/pubpna/US08_NEW_PUB.seq:*
8:  /cgn2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*
9:  /cgn2_6/ptcdata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptcdata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptcdata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptcdata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptcdata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptcdata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptcdata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptcdata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptcdata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptcdata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptcdata/1/pubpna/US60_PUBCOMB.seq:*

| No. | Score | Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 47.6 | 10.2 | 513509 | 10 | US-09-754-853A-4 | Sequence 4, Appli |
| 2 | 47 | 10.1 | 351 | 10 | US-09-814-353-17579 | Sequence 17579, A |
| 3 | 46.8 | 10.1 | 620 | 13 | US-10-424-599-71272 | Sequence 71272, A |
| 4 | 46.2 | 9.9 | 783 | 13 | US-10-424-599-142220 | Sequence 142220, A |
| 5 | 45.8 | 9.8 | 695 | 12 | US-10-401-038-2 | Sequence 2, Appli |
| 6 | 45 | 9.7 | 6071 | 15 | US-10-311-455-340 | Sequence 340, App |
| 7 | 45 | 9.7 | 6071 | 15 | US-10-240-485-36 | Sequence 36, Appl |
| 8 | 44.8 | 9.6 | 337 | 9 | US-09-960-352-6976 | Sequence 6976, Ap |
| 9 | 44.8 | 9.6 | 491 | 13 | US-10-424-599-123899 | Sequence 123899, |
| 10 | 44.8 | 9.6 | 1413 | 13 | US-10-424-599-112225 | Sequence 112225, |
| 11 | 44.8 | 9.6 | 8779 | 15 | US-10-221-613-345 | Sequence 345, App |
| 12 | 44.8 | 9.6 | 3673778 | 15 | US-10-312-841-1 | Sequence 1, Appli |
| 13 | 44.4 | 9.5 | 302 | 10 | US-09-814-353-5335 | Sequence 5335, Ap |
| 14 | 44.4 | 9.5 | 302 | 13 | US-09-814-353-11622 | Sequence 11622, A |
| 15 | 44.4 | 9.5 | 19131 | 13 | US-10-221-714A-441 | Sequence 441, App |
| 16 | 44.2 | 9.5 | 461 | 13 | US-09-814-355-18559 | Sequence 18559, A |
| 17 | 44 | 9.5 | 496 | 13 | US-10-621-901-890 | Sequence 890, App |
| 18 | 43.8 | 9.4 | 577 | 13 | US-10-424-599-135986 | Sequence 135986, |
| 19 | 43.8 | 9.4 | 655 | 13 | US-10-424-599-13378 | Sequence 13378, A |
| 20 | 43.8 | 9.4 | 5511 | 15 | US-10-311-455-1844 | Sequence 1844, Ap |
| 21 | 43.8 | 9.4 | 640681 | 16 | US-09-790-988-1 | Sequence 1, Appli |
| 22 | 43.4 | 9.3 | 970 | 15 | US-10-264-049-91 | Sequence 91, Appli |
| 23 | 43.4 | 9.3 | 3673778 | 15 | US-10-312-841-1 | Sequence 1, Appli |
| 24 | 43.2 | 9.3 | 222 | 13 | US-10-424-599-36762 | Sequence 36762, A |
| 25 | 43.2 | 9.3 | 1358 | 13 | US-10-424-599-65293 | Sequence 65293, A |
| 26 | 43.2 | 9.3 | 3673778 | 15 | US-10-312-841-2 | Sequence 2, Appli |
| 27 | 43 | 9.2 | 406 | 10 | US-09-814-353-4900 | Sequence 4900, Ap |
| 28 | 43 | 9.2 | 406 | 10 | US-09-814-353-11195 | Sequence 11195, A |
| 29 | 43 | 9.2 | 708 | 10 | US-09-814-353-2035 | Sequence 2035, Ap |
| 30 | 43 | 9.2 | 708 | 10 | US-09-814-355-8381 | Sequence 8381, Ap |
| 31 | 43 | 9.2 | 40862 | 15 | US-10-311-455-2045 | Sequence 2045, Ap |
| 32 | 42.8 | 9.2 | 397 | 10 | US-09-814-353-5567 | Sequence 5567, Ap |
| 33 | 42.8 | 9.2 | 397 | 10 | US-09-814-353-11854 | Sequence 11854, A |
| 34 | 42.8 | 9.2 | 473 | 10 | US-09-918-995-13449 | Sequence 13449, A |
| 35 | 42.8 | 9.2 | 746 | 10 | US-09-814-353-5894 | Sequence 5894, Ap |
| 36 | 42.8 | 9.2 | 746 | 10 | US-09-814-353-12175 | Sequence 12175, A |
| 37 | 42.8 | 9.2 | 1061 | 13 | US-10-424-599-100886 | Sequence 100886, |
| 38 | 42.6 | 9.2 | 350 | 10 | US-09-814-353-18240 | Sequence 18240, A |
| 39 | 42.6 | 9.2 | 440 | 10 | US-09-814-355-3227 | Sequence 3227, Ap |
| 40 | 42.6 | 9.2 | 440 | 10 | US-09-814-353-9552 | Sequence 9552, Ap |
| 41 | 42.6 | 9.2 | 579 | 10 | US-09-814-353-5569 | Sequence 5569, Ap |
| 42 | 42.6 | 9.2 | 579 | 10 | US-09-814-355-11856 | Sequence 11856, A |
| 43 | 42.6 | 9.2 | 6731 | 17 | US-10-257-166-44 | Sequence 44, Appl |
| 44 | 42.4 | 9.1 | 377 | 9 | US-09-960-352-7419 | Sequence 7419, Ap |
| 45 | 42.4 | 9.1 | 515 | 13 | US-10-424-599-106126 | Sequence 106126, |

Search completed: April 30, 2004, 11:15:23
Job time : 333 secs

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result    %
          Query

SUMMARIES

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     April 30, 2004, 07:51:05 ; Search time 2507 seconds
                                        5538.857 Million cell updates/sec

Title:              US-09-856-840C-1
Perfect score:      465
Sequence:           1 gactggtaactcattcgat.........taaaaaaaagaaaaaaa 465
Scoring table:      IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0
Searched:           27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:  55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :          EST:*

| | |
|---|---|
| 1: em_estba:* | |
| 2: em_esthum:* | |
| 3: em_estin:* | |
| 4: em_estmu:* | |
| 5: em_estov:* | |
| 6: em_estpl:* | |
| 7: em_estro:* | |
| 8: em_htc:* | |
| 9: gb_esti:* | |
| 10: gb_est2:* | |
| 11: gb_htc:* | |
| 12: gb_est3:* | |
| 13: gb_est4:* | |
| 14: gb_est5:* | |
| 15: em_estfun:* | |
| 16: em_estom:* | |
| 17: em_gss_hum:* | |
| 18: em_gss_inv:* | |
| 19: em_gss_pln:* | |
| 20: em_gss_vrt:* | |
| 21: em_gss_fun:* | |
| 22: em_gss_mam:* | |
| 23: em_gss_mus:* | |
| 24: em_gss_pro:* | |
| 25: em_gss_rod:* | |
| 26: em_gss_phg:* | |
| 27: em_gss_vrl:* | |
| 28: gb_gss1:* | |
| 29: gb_gss2:* | |

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 59 | 12.7 | 452 | 13 | BX446269 | BX446269 BX446269 Drosophil |
| 2 | 56.8 | 12.2 | 1201 | 13 | BX446296 | BX446296 BX446296 |
| 3 | 54.8 | 11.8 | 1162 | 13 | AL513719 | AL513719 AL513719 |
| 4 | 53 | 11.4 | 937 | 29 | AL066056 | AL066056 Drosophil |
| 5 | 52.8 | 11.4 | 1201 | 13 | BX446296 | BX446296 BX446296 |
| 6 | 52.6 | 11.3 | 1045 | 29 | AL266197 | AL266197 Tetraodon |
| 7 | 52.4 | 11.3 | 427 | 13 | BX403499 | BX403499 BX403499 |
| 8 | 52 | 11.2 | 776 | 29 | CNS01G8 | CNS01GC8 |
| 9 | 51.8 | 11.2 | 970 | 29 | CNS0182E | CNS0182E |
| 10 | 51.6 | 11.1 | 179 | 9 | AI275113 | AI275113 ql70e09.x |
| 11 | 51.4 | 11.1 | 1121 | 13 | BX338325 | BX338325 BX338325 |
| 12 | 51.2 | 11.1 | 316 | 14 | CF545414 | CF545414 1ae79a03. |
| 13 | 51.2 | 11.0 | 386 | 13 | C90680 | C90680 C90680 Dict |
| 14 | 51.2 | 11.0 | 392 | 13 | BX424882 | BX424882 BX424882 |
| 15 | 51.2 | 11.0 | 1201 | 13 | BX403761 | BX403761 BX403761 |
| 16 | 51 | 11.0 | 1104 | 9 | AL513809 | AL513809 AL513809 |
| 17 | 50.8 | 10.9 | 392 | 13 | BX424882 | BX424882 BX424882 |
| 18 | 50.8 | 10.9 | 1201 | 9 | AL513975 | AL513975 AL513975 |
| 19 | 50.8 | 10.9 | 1201 | 9 | AL513975 | AL513975 AL513975 |
| 20 | 50.4 | 10.8 | 425 | 14 | CF980658 | CF980658 re07e07.y |
| 21 | 50.4 | 10.8 | 441 | 14 | CF980752 | CF980752 re08f02.y |
| 22 | 50.2 | 10.8 | 409 | 13 | BX425137 | BX425137 BX425137 |
| 23 | 50.2 | 10.8 | 908 | 13 | BX429815 | BX429815 BX429815 |
| 24 | 50.2 | 10.8 | 970 | 29 | CNS0182E | CNS0182E |
| 25 | 50.2 | 10.8 | 1201 | 13 | BX356198 | BX356198 BX356198 |
| 26 | 50 | 10.8 | 501 | 13 | CF302974 | CF302974 7LEAF--08 |
| 27 | 50 | 10.8 | 1162 | 9 | AL513719 | AL513719 AL513719 |
| 28 | 49.8 | 10.7 | 381 | 13 | BX425197 | BX425197 BX425197 |
| 29 | 49.8 | 10.7 | 1201 | 13 | BX458623 | BX458623 BX458623 |
| 30 | 49.6 | 10.7 | 243 | 14 | CF383661 | CF383661 1ac08d05. |
| 31 | 49.6 | 10.7 | 506 | 9 | AL514791 | AL514791 AL514791 |
| 32 | 49.6 | 10.7 | 994 | 29 | CNS04NOJ | CNS04NOJ |
| 33 | 49 | 10.5 | 173 | 12 | BJ423644 | BJ423644 BJ423644 |
| 34 | 49 | 10.5 | 248 | 14 | CF383673 | CF383673 1ac08d07. |
| 35 | 48.8 | 10.5 | 274 | 13 | BX446690 | BX446690 BX446690 |
| 36 | 48.8 | 10.5 | 356 | 13 | BX446758 | BX446758 BX446758 |
| 37 | 48.8 | 10.5 | 625 | 29 | CNS03642 | AL229763 Tetraodon |
| 38 | 48.8 | 10.5 | 658 | 29 | CNS03NK1 | AL252154 Tetraodon |
| 39 | 48.8 | 10.5 | 911 | 13 | BX446782 | BX446782 BX446782 |
| 40 | 48.8 | 10.5 | 240 | 9 | AU073206 | AU073206 AU073206 |
| 41 | 48.6 | 10.5 | 264 | 14 | CF622488 | CF622488 1ae32h01. |
| 42 | 48.6 | 10.5 | 324 | 14 | CF545077 | CF545077 1ad92d04. |
| 43 | 48.6 | 10.5 | 583 | 29 | AL274417 | AL274417 Tetraodon |
| 44 | 48.6 | 10.5 | 716 | 13 | C22772 | C22772 C22772 Dict |

45    48.6    10.5    780    13    BU843635

Search completed: April 30, 2004, 10:10:17
Job time : 2511 secs